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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/478,567	01/06/2000	A. Guruaj Rao	5718-16B	1859

29122 7590 10/21/2004

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EXAMINER	
KALLIS, RUSSELL	

ART UNIT	PAPER NUMBER
1638	

DATE MAILED: 10/21/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/478,567	RAO ET AL.	
	Examiner	Art Unit	
	Russell Kallis	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *09 August 2004*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-3,5-12 and 14-20* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-3,5-12 and 14-20* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *09 August 2004* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *8/24/04;8/14/03*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *attached sequence report*.

DETAILED ACTION

Continued Examination Under 37 CFR 1.114

A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 6/07/2004 has been entered.

Rejection of Claims 1-3, 5-12 and 14-20 under 35 U.S.C. 112 first paragraph, NEW MATTER, is withdrawn in view of Applicant's amendments and arguments.

Rejection of Claims 1-3, 5-12 and 14-20 under 35 U.S.C. 112 first paragraph, written description and enablement, is withdrawn in view of Applicant's amendments and arguments.

Rejection of Claims 1-3, 5-12 and 14-20 under 35 U.S.C 102(e) is withdrawn in view of Applicant's amendments and arguments.

Rejection of Claims 1-3, 5-11 and 14-20 under 35 U.S.C. 103(a) is withdrawn in view of Applicant's amendments and arguments.

The objection to the specification as missing sequence identifiers is withdrawn in view of Applicant's amendments.

Claims 1-3, 5-12 and 14-20 are pending and examined.

Priority

Applicant has not complied with one or more conditions for receiving the benefit of an earlier filing date under 35 U.S.C. 119(e) as follows:

An application in which the benefits of an earlier application are desired must contain a specific reference to the prior application(s) in the first sentence of the specification or in an application data sheet (37 CFR 1.78(a)(2) and (a)(5)). The specific reference to any prior nonprovisional application must include the relationship (i.e., continuation, divisional, or continuation-in-part) between the applications except when the reference is to a prior application of a CPA assigned the same application number. In the first sentence of the specification, Applicant has not indicated that U.S. 09/478,567 is a divisional of U.S. 08/988,015 filed 12/10/1997. Appropriate correction is required.

Information Disclosure Statement

Applicants IDS submitted 8/14/2003 and 8/24/2004 have been reviewed and signed by the Examiner.

Drawings

The drawings were received on 8/09/2004. These drawings are not acceptable. Figures 1A and 1B contain shading that blurs the lettering. Appropriate correction is required.

Specification

The specification is objected to for the following typographical errors:

1) on page 8, line 14, the following is a typographical error "5□–3□".

2) on page 18, line 4, Figure 1 is described as having "blue" color, but the figure is in black and white.

3) on page 21, line 8, the following is a typographical error "37□C".

4) on page 21, line 11, the following is a typographical error "30□C".

Appropriate correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-3, 5-12 and 14-20 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Applicant broadly claims an isolated nucleic acid encoding an engineered VSPα or VSPβ protein of unspecified source and sequence identity having an altered amino acid composition comprising an increase in the essential amino acid composition to at least 5% that binds to at least one antibody, monoclonal antibody, antibody fragment, or protein which binds to the native form of VSPα or VSPβ and plants transformed therewith.

Applicant describes methionine enriched VSPβ variants, VSPβ10 (SEQ ID NO: 8), VSPβ20 (SEQ ID NO: 9), and VSPβ30 (SEQ ID NO: 10) limited to alterations of specific amino acid positions; wild type VSPβ and VSPα from soybean (SEQ ID NO: 1 and SEQ ID NO: 2); an acid phosphatase from tomato (SEQ ID NO: 3) and a pod storage protein PSP from Phaseolis vulgaris (SEQ ID NO: 4); and VSP from *Arabidopsis* (SEQ ID NO: 5-7).

Applicant does not describe an engineered VSPα or VSPβ protein having an altered amino acid composition comprising an increase to at least 5% in the essential amino acid composition of any number of essential amino acids other than VSPβ10 (SEQ ID NO: 8),

VSPβ20 (SEQ ID NO: 9), and VSPβ30 (SEQ ID NO: 10), and that binds to at least one antibody, monoclonal antibody, antibody fragment, or protein which also binds to the native form of VSPα or VSPβ other than VSPβ10 (SEQ ID NO: 8) comprising an increase in the methionine content of native VSPβ to at least 21 of 218 amino acids or 9.6% of the total.

The Federal Circuit has recently clarified the application of the written description requirement to inventions in the field of biotechnology. The court stated that, "A description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus." *See University of California v. Eli Lilly and Co.*, 119 F.3d 1559; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

Applicants fail to describe a representative number of VSPα or VSPβ proteins having an altered amino acid composition comprising an increase in the essential amino acid composition of any number of essential amino acids to at least 5% that binds to at least one antibody, monoclonal antibody, antibody fragment, or protein which also binds to the native form of VSPα or VSPβ. Applicants only describe VSPβ10 (SEQ ID NO: 8) limited to alterations of specific amino acid positions in VSPβ from soybean. Furthermore, Applicants fail to describe structural features common to members of the claimed genus of nucleic acid sequence encoding VSPα or VSPβ proteins having at least 5% increase in essential amino acid content and that bind to at least one antibody, monoclonal antibody, antibody fragment, or protein which also binds to the native form of VSPα or VSPβ. Hence, Applicants fail to meet either prong of the two-prong test set forth by *Eli Lilly*.

Furthermore, given the lack of description of the necessary elements essential for VSPα or VSPβ proteins having at least 5% increase in essential amino acid content that bind to at least one antibody, monoclonal antibody, antibody fragment, or protein which also binds to the native form of VSPα or VSPβ, it remains unclear what features identify the broadly claimed genus. Since the genus of VSPα or VSPβ proteins having at least 5% increase in essential amino acid content that bind to at least one antibody, monoclonal antibody, antibody fragment, or protein which also binds to the native form of VSPα or VSPβ has not been described by specific structural features, the specification fails to provide an adequate written description to support the breath of the claims.

Claims 1-3, 5-12 and 14-20 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for methionine enriched VSP*β* variants, VSP*β*10 (SEQ ID NO: 8), VSP*β*20 (SEQ ID NO: 9), and VSP*β*30 (SEQ ID NO: 10) limited to alterations of specific amino acid positions in VSP*β* and for analogous methionine enriched variants in the VSPα isoform, that bind native VSPα or VSPβ or an antibody specific for native VSPα or VSPβ, and plants transformed therewith, does not reasonably provide enablement for any engineered VSPα or VSPβ protein having altered amino acid composition comprising any number of substitutions at any position within the structure of the native VSPα or VSPβ protein resulting in increases in any number of essential amino acids to at least 5% VSPα or VSPβ that bind to at least one antibody, monoclonal antibody, antibody fragment, or protein which also binds to the native form of VSPα or VSPβ. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make or use the invention commensurate in scope with these claims.

The claimed invention is not supported by an enabling disclosure taking into account the *Wands* factors. *In re Wands,* 858/F.2d 731, 8 USPQ2d 1400 (Fed. Cir. 1988). *In re Wands* lists a number of factors for determining whether or not undue experimentation would be required by one skilled in the art to make and/or use the invention. These factors are: the quantity of experimentation necessary, the amount of direction or guidance presented, the presence or absence of working examples of the invention, the nature of the invention, the state of the prior art, the relative skill of those in the art, the predictability or unpredictability of the art, and the breadth of the claim.

Applicant broadly claims an isolated nucleic acid encoding an engineered VSPα or VSPβ protein of unspecified source and sequence identity having an altered amino acid composition comprising an increase in the essential amino acid composition to at least 5% that binds to at least one antibody, monoclonal antibody, antibody fragment, or protein which binds to the native form of VSPα or VSPβ and plants transformed therewith.

Applicant teaches proposed methionine enriched soybean VSPβ variants, VSPβ10 (SEQ ID NO: 8), VSPβ20 (SEQ ID NO: 9), and VSPβ30 (SEQ ID NO: 10) limited to methionine substitutions at specific amino acid positions in soybean VSPβ (SEQ ID NO: 1) based on mutational analysis of VSPβ, secondary structure prediction of the outer surface protein turns/loops of VSPβ tolerant of amino acid substitutions, and conserved amino acid residues within VSP homologues from *Arabidopsis* (SEQ ID NO: 5-7) and closely related tomato acid phosphatase (SEQ ID NO: 3) and Phaseolus vulgaris pod storage protein PSP (SEQ ID NO: 4) when compared to VSPβ from soybean (specification, pages 13-19 and Figures 1A, 1B and 2); a strategy for isolating correctly folded methionine enriched variants of VSPβ by testing for

binding to a VSPβ specific monoclonal antibody (specification, pages 19-22); and methionine enriched variant VSPβ10 (SEQ ID NO: 8) comprising an increase in the methionine content of native VSPβ to at least 21 of 218 amino acids or 9.6% of the total, binding to wild type VSPβ specific monoclonal antibodies (page 19).

Applicant does not teach an isolated nucleic acid encoding an engineered VSPα or VSPβ protein having altered amino acid composition comprising any number of increases in any essential amino acids to at least 5%, which comprises increases up to 100%, other than the nucleic acid encoding the engineered VSP variants VSPβ10, VSPβ20, and VSPβ30; binding to at least one antibody, monoclonal antibody, antibody fragment, or protein, which binds to the native form of a VSPα or VSPβ protein and plants transformed thereof other than the nucleic acid encoding the engineered VSP variant VSPβ10.

The state-of-the-art is such that one of skill in the art cannot predict whether all or a majority of the residues, or which particular combination of amino acids residues of a protein would tolerate substitution of an essential amino acid or of a methionine to at least 20% content of total amino acids without rigorous trial and error experimental testing. The unpredictability arises from structural constraints that would reduce or eliminate the proteins stability, and hence eliminate the ability to bind to the native protein, given that the native protein binds to itself or a related native isoform, or to an antibody raised against the native protein (Jaynes J.M. Proceedings of Alltech's 10th Annual Symposium, Lexington KY May 1994, pp. 129-153; see page 138 second full paragraph).

Given the lack of guidance in the instant specification, undue trial and error experimentation would be required for one of ordinary skill in the art to make a myriad of

essential amino acid or methionine substitutions into any or all amino acid positions in the sequence of a VSPα or VSPβ protein from soybean or any non-exemplified VSPα or VSPβ protein, in order to increase the essential amino acid content to at least 5% or increase the methionine content to at least 10% or 20%, and test for binding of the engineered protein to any protein that binds the native VSPα or VSPβ protein or for binding to any antibody that binds the native VSPα or VSPβ protein.

Therefore, given the breadth of the claims; the lack of guidance and working examples; the unpredictability in the art; and the state-of-the-art as discussed above, undue experimentation would be required to practice the claimed invention, and therefore the invention is not enabled throughout the broad scope of the claims.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 1-3, 5-12 and 14-20 are rejected under 35 U.S.C. 103(a) as being unpatentable over Staswick P. The Plant Cell, January 1990; Vol. 2, pp.1-6 in view of Dyer J.M. *et al.* Journal of Protein Chemistry, 1995; Vol. 14, No. 8, pp. 665-678.

The claims are broadly drawn to an isolated polynucleotide encoding any VSPα or VSPβ protein engineered to have an increase in essential amino acid content to at least 5% that binds to at least one antibody, monoclonal antibody, antibody fragment, or protein which binds to the

native form of VSPα or VSPβ, and transformed plants and seeds comprising the engineered VSPα or VSPβ sequence.

Staswick teaches that VSPα and VSPβ cDNA and protein sequences from soybean are known in the art; that VSP antisera cross react with specific leaf proteins in several leguminous species (page 4, column 2 3rd paragraph); and teaches that VSP subunits bind to each other as a dimer (page 1 column 2 lines 7-11); and suggests engineering VSPα and VSPβ protein sequences from soybean to increase the availability of nitrogen and sulfur precursors for seed protein synthesis in transgenic plants (see page 4, beginning in the fourth line from the end of column 2 to page 5 column 1, line 18).

Staswick does not teach enrichment of essential amino acid content or methionine content to at least 5%, 10% or 20% by engineering amino acid substitutions into a plant storage protein, that binds to at least one antibody, monoclonal antibody, antibody fragment, or protein which binds to the native form of VSPα or VSPβ, or transformation of legumes or cereals with modified VSP proteins thereof.

Dyer teaches increasing essential amino acid content by substitution of the essential amino acid methionine for genetically variant hydrophobic residues in the β-barrels and loop structures of phaseolin, a seed storage protein from the common bean, wherein the protein maintains its' structural integrity (see Abstract page 665; page 667 next to last line at end of column 1 to line 18 of column 2; and page 670, beginning with Results in column 1 to column 2 of page 670, line 7), an increase in the content of methionine to 23 of 397 total amino acids, increasing essential amino acid content to at least 5% (see page 667, column 2 line 17 and page 674, pMal-PF17 in Table 1); and that legume storage proteins are deficient in methionine and

tryptophan and cereal storage proteins are devoid of lysine and threonine and transformation is a feasible approach to increasing essential amino acid content (page 665 column 2 lines 2-15).

It would have been obvious to modify the invention of Staswick by substituting the essential amino acid methionine for hydrophobic residues as taught by Dyer to increase the essential amino acid content or methionine content of VSPα and VSPβ from soybean to at least 5%, 10% or 20%. One of skill in the art would have been motivated by the teachings of Staswick, that VSPβ from soybean has a hydrophobic amino acid content comprising at least 20% of the total amino acid composition, a lysine content of at least 6.88% (15 of 218 amino acids); that the VSPβ and VSPα protein could be isolated and antisera comprising antibodies raised against VSPβ and VSPα would bind to other plant vegetative proteins; that the VSPα and VSPβ subunits bind each other to form a dimer; and by the teachings of Dyer that the sulfur containing essential amino acid methionine could be substituted for a variety of hydrophobic residues of a plant storage protein and that the engineered protein could maintain its' structural integrity after an increase in in essential amino acid or methionine content to at least 5%, that engineering vegetative storage proteins (i.e. VSPα and VSPβ) would be a valuable tool for engineering increases in essential amino acid or methionine content by plant transformation in leguminous plants, such as soybean, generally deficient in methionine and tryptophan and cereal plants, such as maize, devoid of lysine and threonine; and that one of skill in the art would have a reasonable expectation of success of increasing essential amino acid content of any VSPα and VSPβ protein and having it bind a native VSP specific antibody given the success of Dyer of substituting in methionine for hydrophobic amino acids and thereby increasing the essential amino acid methionine content of phaseolin to at least 5% and maintaining structural stability;

and by the large number of hydrophobic residues available for substitution in either VSPα and VSPβ from soybean allowing further increases in the methionine content to at least 10% or at least 20%; and have a reasonable expectation of success of engineering any native VSP proteins, to have an increase in essential amino acid content to at least 5% that binds to at least one antibody, monoclonal antibody, antibody fragment, or protein which binds to the native form of VSPα or VSPβ, because the native VSP proteins from soybean, taught by Staswick, already comprise an essential amino acid content of at least 40.82% (89 of 218 amino acids, wherein essential amino acids are defined on page 5 of the specification as methionine, tryptophan, lysine, valine, phenylalanine, isoleucine, threonine and cysteine); a lysine content of at least 6.88%(15 of 218 amino acids); a hydrophobic amino acid content comprising more than 20% of the total amino acid composition, and thus provides a native VSP model for engineering any VSPα and VSPβ protein having less than 5% or 10% essential amino acid content to increase essential amino acid content to at least 5% or 10% essential amino acid content or to at least 5% lysine, or to at least 10% or 20% methionine content; and that one of skill in the art would have a reasonable expectation of success in raising antibodies against a native VSP and of transforming soybean and maize.

All claims are rejected.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Russell Kallis whose telephone number is (571) 272-0798. The examiner can normally be reached on M-F 8:30-5.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Amy Nelson can be reached on (571) 272-0804. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Russell Kallis

Russell Kallis Ph.D.
October 6, 2004

Attached Sequence Report

OM protein - protein search, using sw model

Run on: October 6, 2004, 11:33:41 ; Search time 15 Seconds
(without alignments)
756.753 Million cell updates/sec

Title: US-08-988-015-1
Perfect score: 1157
Sequence: 1 RSSEVKCASFRLAVEAHNIR.....GDHRGESRTFKLPNPMYYIE 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1153	99.7	254	1	VSPB_SOYBN	P10743 glycine max
2	939.5	81.2	254	1	VSPA_SOYBN	P15490 glycine max
3	917.5	79.3	291	1	S25K_SOYBN	P10742 glycine max
4	501.5	43.3	255	1	PPA1_LYCES	P27061 lycopersico
5	457.5	39.5	270	1	VSP1_ARATH	O49195 arabidopsis
6	432.5	37.4	265	1	VSP2_ARATH	O82122 arabidopsis
7	110	9.5	274	1	HEL_HAEIN	P26093 haemophilus
8	98.5	8.5	525	1	VL1_HPV5B	P26537 human papil
9	96.5	8.3	491	1	PBP_BACSU	P39844 bacillus su
10	93.5	8.1	516	1	VL1_HPV05	P06917 human papil
11	88	7.6	445	1	G6PB_BACST	P13376 bacillus st
12	87.5	7.6	351	1	CARA_CLOAB	Q97ft2 clostridium
13	87.5	7.6	527	1	ZIM2_HUMAN	Q9nzv7 homo sapien
14	86	7.4	423	1	SNX4_YEAST	P47057 saccharomyc
15	84	7.3	1220	1	DPOL_HSVEB	P28858 equine herp
16	83	7.2	135	1	YJ01_AQUAE	O67739 aquifex aeo
17	83	7.2	360	1	ALF_DROME	P07764 drosophila
18	82.5	7.1	352	1	MUG2_BACAA	Q81je6 bacillus an
19	82.5	7.1	365	1	SERC_LACLA	Q9chw5 lactococcus
20	82.5	7.1	382	1	CAY2_HUMAN	Q9bxy5 homo sapien
21	82.5	7.1	409	1	THBG_RAT	P35577 rattus norv
22	82	7.1	689	1	L100_ADECC	Q65957 canine aden
23	81.5	7.0	516	1	VL1_HPV36	P50812 human papil
24	81.5	7.0	1006	1	BGAL_LACDE	P20043 lactobacill
25	81	7.0	502	1	Y752_BORBU	O51693 borrelia bu
26	81	7.0	522	1	HEX1_ENTHI	P49009 entamoeba h
27	81	7.0	1738	1	YCF1_EPIVI	Q00383 epifagus vi
28	80.5	7.0	544	1	PUS1_YEAST	Q12211 saccharomyc
29	80.5	7.0	562	1	AMY2_DICTH	P14898 dictyoglomu
30	80.5	7.0	1202	1	ALAA_ARATH	Q9li83 arabidopsis
31	80	6.9	363	1	MJD1_CHICK	Q9w689 gallus gall
32	79.5	6.9	433	1	ENOB_CHICK	P07322 gallus gall
33	79	6.8	352	1	MUG2_BACCR	Q812t8 bacillus ce
34	79	6.8	448	1	RMUC_ZYMMO	Q9req3 zymomonas m
35	79	6.8	1228	1	ATC_PLAFK	Q08853 plasmodium
36	78.5	6.8	417	1	FEMB_STAEP	Q8cpa8 staphylococ
37	78.5	6.8	656	1	Y691_RICPR	Q9zcn2 rickettsia
38	78.5	6.8	1030	1	Y075_MYCPN	P75556 mycoplasma
39	78	6.7	208	1	UPP_YERPE	Q8zcx9 yersinia pe
40	78	6.7	233	1	ISPD_LACPL	Q88w46 lactobacill
41	78	6.7	751	1	GCP2_CAEEL	P91406 caenorhabdi
42	77.5	6.7	269	1	RIBF_MYCGE	P47391 mycoplasma
43	77.5	6.7	272	1	AAKC_HUMAN	O43741 homo sapien
44	77.5	6.7	470	1	SYE2_RICPR	Q9zct8 rickettsia
45	77.5	6.7	478	1	DISR_AGKRH	P30403 agkistrodon

ALIGNMENTS

RESULT 1
VSPB_SOYBN
ID VSPB_SOYBN STANDARD; PRT; 254 AA.
AC P10743; Q39823;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE STEM 31 kDa glycoprotein precursor (Vegetative storage protein B).
GN VSPB OR VSP27.
OS Glycine max (Soybean).
OC .Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Williams 82;
RA Mason H.S., Guerrero F.D., Boyer J.S., Mullet J.E.;
RT "Proteins homologous to leaf glycoproteins are abundant in stems of
RT darkgrown soybean seedlings. Analysis of proteins and cDNAs.";
RL Plant Mol. Biol. 11:845-856(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RA Staswick P.E.;
RT "Soybean vegetative storage protein structure and gene expression.";
RL Plant Physiol. 87:250-254(1988).
RN [3]
RP SEQUENCE FROM N.A.
RA Rhee Y., Staswick P.E.;
RL Submitted (SEP-1991) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: May function as somatic storage protein during early
CC seedling development.
CC -!- TISSUE SPECIFICITY: Accumulates in the stems of developing soybean
CC seedlings.
CC -!- SIMILARITY: Belongs to the APS1/VSP family.
CC ----------
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CC ----------
DR EMBL; M37529; AAA33938.1; ALT_SEQ.
DR EMBL; M20038; AAA34021.1; -.
DR EMBL; M76980; AAA34022.1; -.
DR PIR; JN0697; UESY27.
DR InterPro; IPR005519; acid_phosphat_B.
DR Pfam; PF03767; acid_phosphat_B; 1.
KW Glycoprotein; Signal; Seed storage protein.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 35
FT CHAIN 36 254 STEM 31 kDa GLYCOPROTEIN.
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).

```
SQ   SEQUENCE   254 AA;  29280 MW;  C9C8274162F9218F CRC64;

  Query Match           99.7%;  Score 1153;  DB 1;  Length 254;
  Best Local Similarity   99.5%;  Pred. No. 7.6e-90;
  Matches  217;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RSSEVKCASFRLAVEAHNIRAFKTIPEECVSPTKDYINGEQFRSDSKTVNQQAFFYASER 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         37 RSSEVKCASFRLAVEAHNIRAFKTIPEECVEPTKDYINGEQFRSDSKTVNQQAFFYASER 96

Qy         61 EVHHNDIFIFGIDNTVLSNIPYYEKHGYGVEEFNETLYDEWVNKGDAPALPETLKNYNKL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 EVHHNDIFIFGIDNTVLSNIPYYEKHGYGVEEFNETLYDEWVNKGDAPALPETLKNYNKL 156

Qy        121 LSLGFKIVFLSGRYLDKMAVTEANLKKAGFHTWEQLILKDPHLITPNALSYKSAMRENLL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 LSLGFKIVFLSGRYLDKMAVTEANLKKAGFHTWEQLILKDPHLITPNALSYKSAMRENLL 216

Qy        181 RQGYRIVGIIGDQWSDLLGDHRGESRTFKLPNPMYYIE 218
              ||||||||||||||||||||||||||||||||||||||
Db        217 RQGYRIVGIIGDQWSDLLGDHRGESRTFKLPNPMYYIE 254


RESULT 2
VSPA_SOYBN
ID   VSPA_SOYBN     STANDARD;      PRT;   254 AA.
AC   P15490;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   STEM 28 kDa glycoprotein precursor (Vegetative storage protein A).
GN   VSPA.
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Williams 82;
RA   Mason H.S., Guerrero F.D., Boyer J.S., Mullet J.E.;
RT   "Proteins homologous to leaf glycoproteins are abundant in stems of
RT   darkgrown soybean seedlings. Analysis of proteins and cDNAs.";
RL   Plant Mol. Biol. 11:845-856(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Rhee Y., Staswick P.E.;
RL   Submitted (SEP-1991) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: May function as somatic storage protein during early
CC       seedling development.
CC   -!- TISSUE SPECIFICITY: Accumulates in the stems of developing soybean
CC       seedlings.
CC   -!- SIMILARITY: Belongs to the APS1/VSP family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M37530; AAA33937.1; -.
DR   EMBL; M76981; AAA33967.1; -.
DR   PIR; A45504; A45504.
DR   PIR; S08511; S08511.
DR   InterPro; IPR005519; acid_phosphat_B.
DR   Pfam; PF03767; acid_phosphat_B; 1.
KW   Glycoprotein; Signal; Seed storage protein.
FT   SIGNAL        1     21       POTENTIAL.
FT   PROPEP       22     34
FT   CHAIN        35    254       STEM 28 kDa GLYCOPROTEIN.
FT   CARBOHYD    129    129       N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ   SEQUENCE   254 AA;  29065 MW;  1B13F66054CEEF8B CRC64;

  Query Match           81.2%;  Score 939.5;  DB 1;  Length 254;
  Best Local Similarity   79.9%;  Pred. No. 6.7e-72;
  Matches  175;  Conservative   21;  Mismatches   22;  Indels    1;  Gaps    1;

Qy          1 RSSEVKCASFRLAVEAHNIRAFKTIPEECVSPTKDYINGEQFRSDSKTVNQQAFFYASER 60
              |: |||||:|||||||||  |:|||||  ||:||:|||:||||||||||:||| :
Db         36 RTPEVKCASWRLAVEAHNIFGFETIPEECVEATKEYIHGEQYRSDSKTVNQQAYFYARDL 95

Qy         61 EVHHNDIFIFGIDNTVLSNIPYYEKHGYGVEEFNETLYDEWVNKGDAPALPETLKNYNKL 120
              ||| | |:| || |||||||||:||||||:|| ||||||||||:||||||||||||||||
Db         96 EVHPKDTFVFSIDGTVLSNIPYYKKHGYGVEKFNSTLYDEWVNKGNAPALPETLKNYNKL 155

Qy        121 LSLGFKIVFLSGRYLDKMAVTEANLKKAGFHTWEQLILKDPH-LITPNALSYKSAMRENL 179
              :|||||:|||||  ||| |||||||||||:|||:||||||     ||||:|||:| || |
Db        156 VSLGFKIIFLSGRTLDKQAVTEANLKKAGYHTWEKLILKDPQDPSTPNAVSYKTAAREKL 215

Qy        180 LRQGYRIVGIIGDQWSDLLGDHRGESRTFKLPNPMYYIE 218
              :|||| ||||||||||||| ||||||||||||||:|||:
Db        216 IRQGYNIVGIIGDQWSDLLGGHRGESRTFKLPNPLYYIQ 254


RESULT 3
S25K_SOYBN
ID   S25K_SOYBN     STANDARD;      PRT;   291 AA.
AC   P10742;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Stem 31 kDa glycoprotein precursor (Vegetative storage protein VSP25)
DE   (Fragment).
GN   VSP25.
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Leaf;
RA   Staswick P.E.;
RT   "Soybean vegetative storage protein structure and gene expression.";
RL   Plant Physiol. 87:250-254(1988).
RN   [2]
RP   REVISIONS.
RA   Staswick P.E.;
RL   Plant Physiol. 89:717-717(1989).
CC   -!- FUNCTION: May function as somatic storage protein during early
CC       seedling development.
CC   -!- TISSUE SPECIFICITY: Accumulates in the stems of developing soybean
CC       seedlings.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M20037; AAA34020.1; -.
DR   PIR; JA0140; UESY25.
DR   PIR; T08848; T08848.
DR   InterPro; IPR005519; acid_phosphat_B.
DR   Pfam; PF03767; acid_phosphat_B; 1.
KW   Glycoprotein; Signal; Seed storage protein.
FT   NON_TER       1      1
FT   SIGNAL       <1      ?
FT   PROPEP        ?     31
FT   CHAIN        32    291       STEM 31 kDa GLYCOPROTEIN.
FT   CARBOHYD    126    126       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   291 AA;  32882 MW;  4E7CAAE3B3C83DC7 CRC64;
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